

DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE CODED FOR BY C. ELEGANS CDNA YK115A6.5.
GN T01D1.6.
OS *Caenorhabditis elegans*.
OC Eukaryota; Metazoa; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloiderinae; *Caenorhabditis*.
OC NCBI_TaxId=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RX MEDLINE=94150718; PubMed=7906398;
RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
RA Lighting J., Lloyd C., McMurry A., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifken L., Roop A., Saunders D., Showkeen R.,
RA Smaldon N., Smith A., Sonhammer E., Staden R., Sulston J.,
RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
RA Watson A., Weinstock L., Wilkinson-Spoat J., Wohlmann P.;
RT *2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RL elegans.;
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Bradshaw H., Wohlmann P.;
RL Submitted (JAN-1997) to the EMBL/Genbank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Waterston R.;
RL Submitted (NOV-1996) to the EMBL/Genbank/DBJ databases.
DS EMBL: U08455; AAB37867.1; -- 599DAC9DCFA81382 CRC64;
OR SEQUENCE 411 AA; 44675 MW;

	Query Match	21.9%	Score 75;	DB 5;	Length 411;	
	Best Local Similarity	37.0%	Pred. No. 0.16;			
	Matches 17;	Conservative	8;	Mismatches 17;	Indels 4;	Gaps 3.
Dd	3 NPCACRCLQSCQGEPPDDLKORACESRCRKLEYDPCVYDTG-ATNQ 47 1 - - - - - : : : : : - : - - - - 2 16 NTCONSLNFCQQOQOOPIVQO--CGSSCDQ-SCQPQCATPSCSAYNQ 258					
RESULT	3					
ID	044606	PRELIMINARY;	PRT,	388 AA.		
AC	044606;					
DT	01-JUN-1998 (TREMBlrel. 06, created)					
DT	01-JUN-1998 (TREMBlrel. 06, last sequence update)					
DT	01-OCT-2000 (TREMBlrel. 15, last annotation update)					
DE	R09B5.5 PROTEIN. GN R09B5.5. OS Caenorhabditis elegans. OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabdilitidae; Rhabditoidea; OC Rhabditidae; Peioderinae; Caenorhabditis. NCBI_TaxId=6239;					
XX	[1]					
RP	SEQUENCE FROM N.A. STRAIN-BRISTOL NZ; MEDLINE=94150718; PubMed=7906398; RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M., Bonfield J., Burton J., Connell M., Copey T., Cooper J., Coulson A., Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L., Jones M., Keshaw J., Kirsten J., Laister N., Latreille P., Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M., RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Showkeen R.,					

RA Shalender N., Smith A., Sonhammer E., Staden R., Sulston J.,
RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
RA Watson A., Welstock L., Wilkinson-Sproat J., Wohlmann P.:
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of *C.
elegans*.";
RL Nature 368:32-38(1994).
RN [2]
RN
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Sammons L., Wohlmann P., Bauer C., Antoniou B., Wilson R.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
RN [3]
RN
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Mairson R.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
DR EMBL: AF039046; AMB94214.1; -. EA9C3A4AEABFE46 CRC64;
SQ SEQUENCE 388 AA: 41440 MW: EA9C3A4AEABFE46 CRC64;

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Query Match:          20.8%   Score 71.5; DB 5; Length 388;
Best Local Similarity 32.1%   Pred. No. 0.4;
Matches 17; Conservative 7; Mismatches 22; Indels 7; Gaps 2

      5 CAORCAGC--GQEPDLKQKACSEKCTKLEYDPCVYDTCATNQRHPGERT 55
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 196 CQOQCCSSCTQOQOCPANQCNACNSQCSNI-----CQDTAATQOYVNSNT 243

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RESULT	4			
ID	016446	PRELIMINARY;	PRF;	221 AA.
AC	016446;			
DT	01-JAN-1998 (Tremblrel. 05, Created)			
DT	01-JAN-1998 (Tremblrel. 05, Last sequence update)			
DT	01-NOV-1998 (Tremblrel. 08, Last annotation update)			
DE	C5AF6.6 PROTEIN.			
GN	C5AF6.6			
OS	Caenorhabditis elegans.			
OC	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;			
OC	Rhabditidae; Petaloderinae; Caenorhabditis.			
OX	NCBI_TaxID=6239;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-BRISTOL N2;			
RC	MEDLINE=94150718; Pubmed=790638;			
RA	Wilson R., Ainscough R., Anderson K., Baynes C., Berks M., Coulson A.,			
RA	Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,			
RA	Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,			
RA	Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,			
RA	Jones M., Kershaw J., Kristen J., Laister N., Latreille P.,			
RA	Lightning J., Lloyd C., McMurry A., Mortimore B., O'Callaghan M.,			
RA	Parsons J., Percy C., Ritken L., Roopra A., Saunders D., Showkeen R.,			
RA	Smalton N., Smith A., Sonhammer E., Staden R., Sulston J.,			
RA	Thierry-Mieg J., Thomas K., Vaudin R., Vaughan K., Waterston R.,			
RA	Watson A., Wellstoun L., Wilkinson-Sproat J., Wohlman P.;			
RT	2.2 Mb of contiguous nucleotide sequence from chromosome III of C.			
RT	elegans.";			
RL	Nature 368:32-38(1994).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-BRISTOL N2;			
RC	Geisel C., Bradshaw H.;			
RA	Submitted (Aug-1997) to the EMBL/Genbank/DBJ databases.			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-BRISTOL N2;			
RA	Waterston R.;			
RA	Submitted (JUL-1997) to the EMBL/Genbank/DBJ databases.			
EMBL:	AF016447; AAB65937.1; -			
Q0	SEQUENCE 221 AA; 25043 MW; FC904099EA3EB87C CRC64;			

Query Match	20.4%	Score 70;	DB 5;	Length 221;
Best Local Similarity	29.6%;	Pred. NO. 0.37;		
Matches 16;	Conservative 7;	Mismatches 15;	Indels 16;	Gaps 2;

```
Oy      3 NPCAQRCLQSCQQEPDDLKQACESRCKLEY-----DPRCYVD 41
         | || :| : |:| ||:| || :          : |||| 
Db     165 NNCAPKCFSSSPDKKDENVLK-CETTKAKLRFTMEEDDAKFSPFENCNQACYVD 21
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RESULT	5	
Q27383		
ID	Q27383	PRELIMINARY;
AC	Q27383	PRT; 378 AA

DT	01-JUN-1998	(TEMBLrel. 06, Created)
DT	01-JUN-1998	(TEMBLrel. 06, last sequence update)
DT	01-JUN-1998	(TEMBLrel. 06, last annotation update)
DE	HYPOHETICAL 40-7 KDA PROTEIN R09F10.2 IN CHROMOSOME X PRECURSOR.	
GN	R09F10.2 AND R09F10.7.	
OS	Caenorhabditis elegans.	
OC	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidae	
OC	Rhabditidae; Pelodierinae; Caenorhabditis.	
OX	NCBI_TaxId=6239;	
RP	[1]	
RC	SEQUENCE FROM N.A.	
SC	STRAIN-BRISTOL N2.	
RA	Couch J.;	
RL	Submitted (JUL-1996) to the EMBL/Genbank/DBJ databases.	
CC	- SIMILARITY: BELONGS TO FAMILY UPE.	
DR	EMBL: U64859; AACG9090.1; -	
DR	EMBL: U64859; AACG9096.1; -	
DR	MORMREP: R09F10.2; CE07436.	
DR	MORMREP: R09F10.7; CE07441.	
KM	Hypothetical protein; signal.	
FT	SIGNAL	
FT	CHAIN 19 378 POTENTIAL.	
QO	SECUDNCE 378 AA; 40663 MW; E38BA16BEF3A7610 CRC54; HYPOHETICAL PROTEIN R09F10.2.	

Query Match	20.4%;	Score 70;	DB 5;	Length 378;
Best Local Similarity	37.8%;	Pred. No. 0.6;		
Matches 14; Conservative	6;	Mismatches 11;	Indels 6;	Gaps 2;

QY 5 CAORCLSCQDEP-----DLKQKACESRCTKLEYDP 36
| | | | | : | : | : | : | :
Db 84 CQDSCRQCGSAPAVSQGQPWMCQQQCQSCTPM-YNP 119

RESULT	6
Q9SPL3	
ID	Q9SPL3
PRELIMINARY;	
PRT;	625 AA

DT 01-MAY-2000 (TREMBLREL. 13, Created)
DT 01-MAY-2000 (TREMBLREL. 13, Last sequence update)
DT 01-OCT-2000 (TREMREL. 15, Last annotation update)
DE VICILIN PRECURSOR (FRAGMENT).

OS *Macadamia integrifolia* (Macadamia nut).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 CC Magnoliophyta; eudicotyledons; Proteaceae; Macadamia.
 NCBI_TaxID=60698;
 OX

RC SEQUENCE FROM N.A.
RP TISSUE-NUT KERNEL;
RA Marcus J.P., Goulter K.C., Green J.L., Manners J.M.;
RT "A family of antimicrobial peptides is produced by processing of a 7S

RT globulin protein in Macadamia integrifolia.";
RL Plant J. 0:0-0(1999).
DR EMBL; AF11885; AAD54246.1; -.
DR HSSP; P02853; 2PHI.
INTERPRO: IPR001113. -

DR	PFAM:	Seedstore_7s; 1.
FT	NON_TER	1
SQ	SEQUENCE	625 AA; 73586 MW; 415808A89D370296 CRC64;

	Query Match	20.3%	Score 69.5;	DB 10;	length 625;
	Best Local Similarity	30.0%	Pred. No. 1.1;		
	Matches , 12; Conservative	10;	Mismatches	11;	Indels 7; Gaps 1;
QY	5 CACRCLSCGCGEPDDLK-----AECSTKLEIYPR	37			
	I : I I : I : I : I : I : I : I : I : I :				
Dd	61 CORCKETCEEEENRRDPDPOOCTEGCCRKCRRETER	100			

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QY      5 CAORCLSCQGFDDDKOK-----ACESRCKLEYIPR 37
          |::|::|::|::|::|::|::|::|::|::|
Db      61 CQRCKELCEEELYYNRQDPQQYEQCGKRCQRETER 100
```

RESULT	7	
Q49549		
ID	Q49549	PRELIMINARY;
NC	Q49549	PRT; 1187 AA.

DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)
 DT 01-NOV-1998 (TREMBLrel. 08, last annotation update)
 DE REPEAT REGIONS IN POTENTIAL METAL BINDING PROTEIN GENE REGION
 OS Mycoplasma hyorhinis.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Molluscites;
 OC Mycoplasmataceae; Mycoplasma.
 OX NCBI_TaxID=2100;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=GD1;
 RX MEDLINE=95014025; PubMed=7928953;
 RA Deng G., McIntosh M. A.;
 RT "An amplifiable DNA region from the Mycoplasma hyorhinis genome
 J. Bacteriol. 176:5929-5937(1994).
 EMBL: L11447; AA62228.1;
 SQ SEQUENCE 1187 AA; 135027 MW; 66A82AE5B0DE93E CRC64;

Query Match	20.1%	Score 69	DB 2	Length 1187
Best Local Similarity	28.6%	Pred. No. 2.2		
Matches	20	Conservative 12	Mismatches 22	Indels 16
				Gaps 5

OY 1 TENPCAQRCLQS---CQEPDDLKOKKC---ESRCKTLEYDPRCV-----YDT---GATN 46
|| | : | : || | : ||
Db 403 TEHC- -ECTESTGCCENPECEFEACDCSEHHCCEVDETQACIDCNTQADTKVCCTQ 460

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QY      47 QRHPPGERTR 56
          ::||| | :
Db      461 EQHPJTCEECK 470
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RESULT	8	.
Q9SPL4		
ID	Q9SPL4	PRELIMINARY;
		PRT;
		666 AA.

DT	01-MAY-2000	(Tremblurel. 13, Created)
DT	01-MAY-2000	(Tremblurel. 13, last sequence update)
DT	01-OCT-2000	(Tremblurel. 15, last annotation update)
DE	VICILIN PRECURSOR.	

OS *Macadamia integrifolia* (Macadamia nut).
 OC Eukaryota: Viridiplantae: Embryophyta: Tracheophyta: Spermatophyta.
 MC Magnoliophyta: eudicotyledons: Proteaceae: Macadamia.
 OX NCBI_TaxID=60698;

RP SEQUENCE FROM N.A.
RC TISSUE=NOT KERNEL;
RA Marcus J.P., Goulter K.C., Green J.L., Manners J.M.;
RT "A family of antimicrobial peptides is produced by processing of a 7S

RT globulin protein in Macadamia integrifolia.",
 RL Plant J. 0:0-0(1999).
 EMBL: AF161884; AAD54245.1; -.
 DR HSSP: P02853; 2PHT.
 WWW: www.ncbi.nlm.nih.gov/blast/

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DR PFAM: PF00546; Seedstore_7s: 1.  
SQ SEQUENCE 666 AA; 78243 MW; 0ECA22F8710F8A7B CRC64;
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Query Match          20.0%; Score 68.5; DB 10; Length 666;
Best Local Similarity 30.0%; Pred. No. 1.5;
Matches 12; Conservative 10; Mismatches 11; Indels 7; Gaps 1;

OY 5 CAORCLOSCQOEPPDLKOK-----ACESRCKLEYDPR 37
DB 102 CORRKEICEEEYNNRDPDQOYECOCERCORHTEPR 141

RESULT 9
O17970 PRELIMINARY; PRT; 1513 AA.
AC 017970;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DE 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE M0269.1 PROTEIN.
GN M0269.1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Matthews L.;
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RX MEDLINE=94150718; PubMed=7906398;
RA Wilson R., Almscough R., Anderson K., Baynes C., Berks M.,
RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
RA Jones M., Kershaw J., Kirsten J., Laister N., Latrelle P.,
RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Ritken L., Roopra A., Saunders D., Shownkeen R.,
RA Smaildon N., Smith A., Sonhammer E., Staden R., Sulston J.,
RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
RA Watson A., Weinstock L., Wilkison-Sproat J., Wohlman P.;
RT *2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans.
RL Nature 368:32-38(1994).
DR EMBL; 281573; CAB04625.1; -.
DR HSSP; 046655; 1CJH.
SQ SEQUENCE 1513 AA; 161578 MW; 10BCB4287BA282E5 CRC64;

Query Match          20.0%; Score 68.5; DB 5; Length 1513;
Best Local Similarity 28.8%; Pred. No. 3.2;
Matches 15; Conservative 9; Mismatches 11; Indels 17; Gaps 3;

OY 4 PCAORCLOSCQOE-----PDLKOKACESRCKLEYDPRCYDNGAT 45
DB 405 PCORCLOSCLEHIOHPQVYTOIPQICPO-----EPQCIQETITTT 449

RESULT 10
O16502 PRELIMINARY; PRT; 438 AA.
AC 016502;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DE 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE C03A7.8 PROTEIN.
GN C03A7.8.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=BRISTOL N2;
RC STRAIN=BRISTOL N2;

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RX MEDLINE=94150718; PubMed=7906398;
RA Wilson R., Almscough R., Anderson K., Baynes C., Berks M.,
RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
RA Jones M., Kershaw J., Kirsten J., Laister N., Latrelle P.,
RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Ritken L., Roopra A., Saunders D., Shownkeen R.,
RA Smaildon N., Smith A., Sonhammer E., Staden R., Sulston J.,
RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
RA Watson A., Weinstock L., Wilkison-Sproat J., Wohlman P.;
RT *2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans.
RL Nature 368:32-38(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Greco T., Bradshaw H., Elliott G.;
RN Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RX SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Waterston R.;
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF016431; AAB65995.1; -.
SQ SEQUENCE 438 AA; 47502 MW; 835C4F68ECF510B1 CRC64;

Query Match          19.7%; Score 67.5; DB 5; Length 438;
Best Local Similarity 33.3%; Pred. No. 1.4;
Matches 15; Conservative 7; Mismatches 16; Indels 7; Gaps 2;

OY 5 CAORCLOSC--QOEPPDLKOKACESRCKLEYDPRCYDNGATNQ 47
DB 201 CQOQCOSSCWQOQDPNQCPCPACNTQCSD-----CQQTQAATQO 240

RESULT 11
O16511 PRELIMINARY; PRT; 445 AA.
AC 016511;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DE 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE C03A7.14 PROTEIN.
GN C03A7.14.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RX MEDLINE=94150718; PubMed=7906398;
RA Wilson R., Almscough R., Anderson K., Baynes C., Berks M.,
RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
RA Jones M., Kershaw J., Kirsten J., Laister N., Latrelle P.,
RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Ritken L., Roopra A., Saunders D., Shownkeen R.,
RA Smaildon N., Smith A., Sonhammer E., Staden R., Sulston J.,
RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
RA Watson A., Weinstock L., Wilkison-Sproat J., Wohlman P.;
RT *2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans.
RL Nature 368:32-38(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Greco T., Bradshaw H., Elliott G.;
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
RN [3]

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RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA Waterston R.;
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases
DR EMBL: AF016451; AAB66007.1; -
SQ SEQUENCE 445 AA; 48202 MW; A65C08DDC136B8ADA CXC64;

Query Match	19.7%	Score	67.5;	DB	5;	Length	445;
Best Local Similarity	33.3%	Pred. No.	1.4;				
Matches	15;	Conservative	7;	Mismatches	16;	Indels	7;
						Gaps	2

QY 5 CAQRCLQSC--QGEPPDLKQKACESRCTKLEIDPRCVYDTGATNQ 47
 ||:| || ||:| :||:|:| :|||
 Db 201 CQ0QCQSSCV000QPSQCEPACNTQCSDI-----CQQTAAQTQQ 240

RESULT 12	
Q9UDQ1	
ID Q9UDQ1	PRELIMINARY;
Q9UDQ1	PRT; 287 AA.

DT	01-MAY-2000 (TREMblrel. 13, created)
DT	01-MAY-2000 (TREMblrel. 13, last sequence update)
DT	01-JUN-2000 (TREMblrel. 14, last annotation update)
DE	SEQUENCING ITI PROTOCOL (ndc10000)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;

RP SEQUENCE FROM N.A.
RX MEDLINE=99063792; PubMed=9847074;
RA Sulston J.E., Waterston R.;
RT "Toward a complete human genome sequence.";
RL Genome Res. 8:1097-1108(1998).

RP SEQUENCE FROM N.A.
RA Holmes A., Gregory S.;
RT "The sequence of Homo sapiens PAC clone RP5-1060B1.";
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases

KN 13] SEQUENCE FROM N.A.
 RP Waterston R.H.;
 RA Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases
 RN [4]
 RP SEQUENCE FROM N.A.

RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases
DR EMBL; AC006322; AAD20933.1; -.
DR INTERPRO; IPR003006; -.

```
DR      PFAM; PF00047; ig; 1.
FT      NON_TER      1
SQ      SEQUENCE      287 AA; 33548 MW; CBC66E2E94AD573F CRC64;
```

Query Match	19.4%;	Score 66.5;	DB 4;	Length 287;
Best Local Similarity	35.2%;	Pred. No. 1.3;		
Matches 19; Conservative	5;	Mismatches 23;	Indels 7;	Gaps 2

QY 6 AQRCLSCQQEPPDDLKQACESCRKLEYDPRCVYDTGATNQRHPGERTGRQ 59
| | : | | | | : | : |
Db 26 AQPLHRC----DIYGKACAEC--LARDPYCAMDGASCSRYFTAKRRTRQ 72

RESULT	13	
ID	Q19919	PRELIMINARY;
	Q19919	PRT;
	Q19919	242 AA.

DT 01-JUN-1998 (TREMBLrel..06, Created)
DT 01-JUN-1998 (TREMBLrel..06, Last sequence update)
DT 01-JUN-1998 (TREMBLrel..06, Last annotation update)
DE HYPOTHEICAL 26.2 KDA PROTEIN F3IA3.1 IN CHROMOSOME X.
GN F3IA3.1.

OS *Caenorhabditis elegans*.
 OC Eukaryota; Metazoa; Nematoda; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Pelodierinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 113

RC STRAIN=BRISTOL N2;
RA Murray J., Le T. T. J;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases
-1- SIMILARITY, REFERENCES AND PATENT INFO

KW	Hypothetical protein; Transmembrane.
FT	TRANSMEM 3 23 POTENTIAL.
SO	SEQUENCE 242 AA; 26213 MW; C7D6996BD0829317 CRC64

Query Match	19.2%	Score 66:	DB 5;	Length 242;
Best Local Similarity	43.3%	Pred. No.	1.2;	
Matches 13;	Conservative 3;	Mismatches 12;	Indels 2;	Gaps 1

QY 2 ENPCACRCLQSCQGEPPDLKQKACESRCK 31
| | | | | : : : | | | |
Db 175 EPQCQSCQCCVCQQQDSMQ--CASACTK 202

RESULT	14	
016500		
ID	016500	PRELIMINARY; PRT; 388 AA.

DE C03A7.4. PROTEIN.
DN C03A7.4.
DT 01-JAN-1998 (TREMblrel. 05, Created)
DT 01-JAN-1998 (TREMblrel. 05, Last sequence update)
DT 01-NOV-1998 (TREMblrel. 08, Last annotation update)
C03A7.4. PROTEIN.
C03A7.4.

OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabdittia; Rhabdittioidea
OC Rhabdittidae; Pelodierinae; Caenorhabdittis.
OX NCBI_TaxID=6239;
RN [1]

RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2.
RX MEDLINE=94150718; PubMed-7906398;
RA Wilson R., Almscough R., Anderson K., Baynes C., Berks M.,
RA Bonfield J., Burton J., Connell M., Copesey T., Cooper J., Coulson A.,
RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,

RA Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Showkeen R.,
RA Jones M., Keshaw J., Kirsten J., Laister N., Latreille P.,
RA Lightning J., Lloyd C., McMurray A., Morfimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Showkeen R.,

RA Smaildon N., Smith A., Sonnhamer E., Staden R., Sulston J.,
RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
RA Watson A., Weinstein L., Wilkinson-Sproat J., Wohlman P.,

RL Nature 368:32-38 (1994).
RN [2]
RP SEQUENCE FROM N. A.

RA Greco T., Bradshaw H., Elliott G.;
RL Submitted (Aug-1997) to the EMBL/GenBank/DBJ databases
RN [3]

RA Waterston R.;
 RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases
 DR EMBL; AF016451; AAB66001.1; -.

Query Match	19.2%;	Score 66;	DB 5;	Length 388;
Best Local Similarity	43.8%;	Pred. No. 1.9;		
Matches 14;	Conservative	4;	Mismatches	8;
			Indels	6;
			Gaps	1;

QY 5 CAQRCLOSC-----QQEPDDLKQKACESRCT 30
 DB 317 CAPOCEOSCOQCCVQ00QPAACCTACQSSCS 348

RESULT 15

016501 PRELIMINARY; PRT; 388 AA.
 AC 016501;
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
 DE C03A7.7 PROTEIN.
 GN C03A7.7.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RX MEDLINE=94150718; PubMed=7906398;
 RA Wilson R., Almscough R., Anderson K., Baynes C., Berks M.,
 RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
 RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
 RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
 RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
 RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
 RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Showkeen R.,
 RA Smaison N., Smith A., Sonhammer E., Staden R., Sulston J.,
 RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
 RA Watson A., Wellstock L., Wilkinson-Sproat J., Wohlman P.,
 RA "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 RT elegans.";
 RL Nature 368:32-38(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA Greco T., Bradshaw H., Elliott G.,
 RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA Waterston R.,
 RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF016451; AAB65996.1; -
 SQ SEQUENCE 388 AA; 42129 MW; 74ACA3953E0AF2A2 CRC64;

Query Match 19.2%; Score 66; DB 5; Length 388;
 Best local Similarity 43.8%; Pred. No. 1.9;
 Matches 14; Conservative 4; Mismatches 8; Indels 6; Gaps 1;
 QY 5 CAQRCLOSC-----QQEPDDLKQKACESRCT 30
 DB 317 CAPOCEOSCOQCCVQ00QPAACCTACQSSCS 348

Search completed: March 1, 2001, 16:09:38
 Job time: 1582 sec